



TECH CENTER

ENCLOSED

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,744B

DATE: 04/21/2003

TIME: 17:03:14

Input Set : N:\paola\09905744B.txt

Output Set: N:\CRF4\04212003\I905744B.raw

3 <110> APPLICANT: Chadwick, Brian Paul
 4 Frischauf, Anna Maria
 5 <112> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
 AND NUCLEIC

7 ACIDS

9 <120> FILE REFERENCE: 38110/36120A

11 <140> CURRENT APPLICATION NUMBER: 09/905,744B

12 <141> CURRENT FILING DATE: 2001-07-13

14 <150> PRIOR APPLICATION NUMBER: 09/240,639

15 <151> PRIOR FILING DATE: 1999-01-29

17 <160> NUMBER OF SEQ ID NOS: 32

19 <170> SOFTWARE: PatentIn version 3.1

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 2762

23 <212> TYPE: DNA

24 <213> ORGANISM: Homo Sapiens

26 <216> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (132)..(1599)

29 <223> OTHER INFORMATION:

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35 ggcgggtgca tgaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttcaga 180
36 aaaaagagct acatttttca gcagccgcag cagggtcctt ggcaacaag g atg aga 237
37 Met Arg
38 1
39 aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
40 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
41 5 10 15
42 cgg ggg ctg tct gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
43 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
44 20 25 30
45 car ggg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
46 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
47 35 40 45 50
48 ccc ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
49 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
50 55 60 65
51 gca gac gcc cac gag gtc ttc tac ggt atc atg ttt gat gca gga agc 477
52 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
53 70 75 80
54 acr ggc acc aga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525
55 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu

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65	85	90	95	
67 act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt				573
68 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu				
69 100	105	110		
71 tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa				621
72 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu				
73 115	120	125	130	
75 cta ctg gat gtt gct aaa cag gac att cgg ttc gac ttc tgg aag gcc				669
76 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala				
77 135	140	145		
79 acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga				717
80 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly				
81 150	155	160		
83 gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca				765
84 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala				
85 165	170	175		
87 tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca				813
88 Ser Pro Phe Leu Val Gly Asp Cys Val Ser Ile Met Asn Gly Thr				
89 180	185	190		
91 gat gaa ggc gtt tcg ggg tgg atc acc atc aac ttc ctg aca ggc agc				861
92 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser				
93 195	200	205	210	
95 ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga				909
96 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly				
97 215	220	225		
99 gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag				957
100 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln				
101 230	235	240		
103 gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc				1005
104 Ala Ser Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr				
105 245	250	255		
107 tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcc gca				1053
108 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala				
109 260	265	270		
111 cgc ctg ggc atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga				1101
112 Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly				
113 275	280	285	290	
115 aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg				1149
116 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp				
117 295	300	305		
119 gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca ggc gca				1197
120 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala				
121 310	315	320		
123 agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac				1245
124 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn				
125 325	330	335		
127 aga gtg cac agc acg gag gaa gtg aag cat gtg gac ttc tat gct ttc				1293
128 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe				
129 340	345	350		

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131 tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag      1341
132 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
133 355          360          365          370
134 aag gaa gga agc ctg ctg gtg ggg gac ttc gag atc gca gcc aag tac      1389
135 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
136          375          380          385
137 gtt tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc      1437
138 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
139          390          395          400
140 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc      1485
141 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
142          405          410          415
143 agc agc aaa ctg ctg aag ctc act cgg aaa att gac aat gtt gag acc      1533
144 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
145          420          425          430
146 agc tgg gct ctg cgg gcc att ttt cat tac atc gac tcc ctg aac aga      1581
147 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
148          435          440          445          450
149 cag aag agt cca gcc tca tagtggeega gccatccctg tccccgtcag      1629
150 Gln Lys Ser Pro Ala Ser
151          455
152 cagtgtctgt gtgtctgcat aaacccctct gtccctggacg tgacttcato ctgaggagcc      1689
153 acagcacagg ccgtgtggc actttctgca cactggtctt gggacttgca gaaggccctgg      1749
154 tctgtccctg gcatcagcct ctccacagtea catctggcca gagggtctgc tggacctggg      1809
155 cccctgtctaa tgccacctgt ctgcccgggc tccaaagtggg caggaccagg acagaaccac      1869
156 aggcacacac tgagggggga gtgtggtctc ctgcccgttc catcccatg ccccgctccg      1929
157 ggggtgtgtg ctgctctctgt gcatgtccct gcataggag tcttgtctcc cagcctgtea      1989
158 gtttctctcc cagggcagag ctccccttcc tgcaagagtc tgggaggcgg tgcaggctgt      2049
159 cctggctgct ctggggaagg cgaaggacag ccataacacc cccgggacag taggtctggg      2109
160 cggcaccaact gggaactctg gacttgagtg tgtttgtctt tccctgggta tgaatgtgtg      2169
161 agttcaccac gaggcctgct ctctcaccac attgtgtggt ttgggggtta tgaatgtgtg      2229
162 agacacctct tcatagacgg caggtgccca cctttcaggg agtctccag catgggggga      2289
163 tcccgggcat gacgtgctgt aaactatctt tggtgtgtgt gcttgagtga cgtctctgtc      2349
164 gtgtgggtac caagtgtctg tctagaaact gtgttctgag cccctcttcc tggacaccac      2409
165 ctgtctctct tgaatgtat gctactgtga gtgttcccg cctagccagg gccatgtctt      2469
166 aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctgggtgtct      2529
167 cgggcacaca tccgcacacc tccggctgac cccacccctt ccatggacag tgtgagcccc      2589
168 cggcgtgca tccgtctcag tctgggtcga gtgtcggggc tgagccctct gacgtgtctc      2649
169 agtgaatgta cagtgcctgg cagagctga acctcatgtg ttccactccc aataaaaagg      2709
170 tgacaggggc tctctcttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa      2762
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172 <110> SEQ ID NO: 2
173 <111> LENGTH: 456
174 <112> TYPE: PRT
175 <113> ORGANISM: Homo Sapiens
176 <114> SEQUENCE: 2
177 Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
178 1          5          10          15
179 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
180 20          25          30

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Output Set: N:\CRF4\04212003\I905744B.raw

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213 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
214      35      40      45
217 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
218      50      55      60
221 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
222 65      70      75      80
225 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
226      85      90      95
229 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
230      100     105     110
233 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
234      115     120     125
237 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
238      130     135     140
241 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
242 145      150     155     160
245 Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
246      165     170     175
249 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
250      180     185     190
252 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
254      195     200     205
257 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
258      210     215     220
261 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
262 225      230     235     240
265 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
266      245     250     255
269 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
270      260     265     270
273 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
274      275     280     285
277 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
278      290     295     300
281 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
282 305      310     315     320
285 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
286      325     330     335
289 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
290      340     345     350
293 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
294      355     360     365
297 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
298      370     375     380
301 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
302 385      390     395     400
305 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
306      405     410     415
309 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val

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310          420          425          430
311 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
314          435          440          445
317 Asn Arg Gln Lys Ser Pro Ala Ser
318          450          455
321 <210> SEQ ID NO: 3
322 <210> LENGTH: 1797
323 <210> TYPE: DNA
324 <210> ORGANISM: Homo Sapiens
326 <210> FEATURE:
327 <210> NAME/KEY: CDS
328 <210> LOCATION: (83)..(1669)
329 <210> OTHER INFORMATION:
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336 ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt      112
337          Met Phe Thr Val Leu Thr Arg Gln Pro Cys
337          1          5          10
339 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc      160
340 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
341          15          20          25
343 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc      208
344 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
345          30          35          40
347 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt      256
348 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
349          45          50          55
351 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa      304
352 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
353          60          65          70
355 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc      352
356 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
357 75          80          85          90
359 aaa tgt agt gtg aaa ggc tct gga atc tcc ago tat gga aat aac ccc      400
360 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
361          95          100          105
363 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg      448
364 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
365          110          115          120
367 cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc      496
368 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
369          125          130          135
371 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat      544
372 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
373          140          145          150
375 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac      592
376 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
377 155          160          165          170
379 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga      640

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VERIFICATION SUMMARYPATENT APPLICATION: **US/09/905,744B**

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Input Set : **N:\paola\09905744B.txt**Output Set: **N:\CRF4\04212003\I905744B.raw**

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L:332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:329
L:664 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:661
L:924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:921